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<!--StartFragment-->RESULT 1
KIRR2_MOUSE
ID      KIRR2_MOUSE          Reviewed;          700 AA.
AC      Q7TSU7; Q7TQ98;
DT      25-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT      01-OCT-2003, sequence version 1.
DT      24-JUL-2007, entry version 34.
DE      Kin of IRRE-like protein 2 precursor (Kin of irregular chiasm-like
DE      protein 2).
GN      Name=Kirrel2;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muroidea; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC      TISSUE=Olfactory epithelium;
RX      PubMed=15489334; DOI=10.1101/gr.2596504;
RG      The MGC Project Team;
RT      "The status, quality, and expansion of the NIH full-length cDNA
RT      project: the Mammalian Gene Collection (MGC).";
RL      Genome Res. 14:2121-2127(2004).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [MRNA] OF 48-376 (ISOFORM 2), AND TISSUE
RP      SPECIFICITY.
RX      MEDLINE=22721688; PubMed=12837264; DOI=10.1016/S0888-7543(03)00110-1;
RA      Sun C., Kilburn D., Lukashin A., Crowell T., Gardner H., Brundiers R.,
RA      Diefenbach B., Carulli J.P.;
RT      "Kirrel2, a novel immunoglobulin superfamily gene expressed primarily
RT      in beta cells of the pancreatic islets.";
RL      Genomics 82:130-142(2003).
RN      [3]
RP      INTERACTION WITH NPHS2, AND TISSUE SPECIFICITY.
RC      STRAIN=Swiss Webster; TISSUE=Brain;
RX      PubMed=12424224; DOI=10.1096/fj.02-0242fje;
RA      Sellin L., Huber T.B., Gerke P., Quack I., Pavenstaedt H., Walz G.;
RT      "NEPH1 defines a novel family of podocin interacting proteins.";
RL      FASEB J. 17:115-117(2003).
CC      -!- SUBUNIT: Interacts with C-terminus of NPHS2/podocin.
CC      -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I membrane
CC      protein (Potential).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q7TSU7-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q7TSU7-2; Sequence=VSP_011786;
CC      -!- TISSUE SPECIFICITY: Highly expressed in beta-cells of the
CC      pancreatic islets. Expressed also in podocytes of kidney
CC      glomeruli.
CC      -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC      -!- SIMILARITY: Contains 5 Ig-like C2-type (immunoglobulin-like)
CC      domains.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; BC052773; AAH52773.1; -; mRNA.
DR      EMBL; AY305303; AAP72168.1; -; mRNA.
DR      UniGene; Mm.113908; -.

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DR Ensembl; ENSMUSG00000036915; Mus musculus.
 DR MGI; MGI:2442334; Kirrel2.
 DR InterPro; IPR013162; CD80_C2-set.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR013783; Ig-like_fold.
 DR InterPro; IPR013098; Ig_I-set.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR003598; Ig_sub2.
 DR InterPro; IPR013106; Ig_V-set.
 DR Gene3D; G3DSA:2.60.40.10; Ig-like_fold; 3.
 DR Pfam; PF08205; C2-set_2; 1.
 DR Pfam; PF07679; I-set; 2.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 PE 1: Evidence at protein level;
 KW Alternative splicing; Glycoprotein; Immunoglobulin domain; Membrane;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 700 Kin of IRRE-like protein 2.
 FT /FTId=PRO_0000015097.
 FT TOPO_DOM 20 507 Extracellular (Potential).
 FT TRANSMEM 508 528 Potential.
 FT TOPO_DOM 529 700 Cytoplasmic (Potential).
 FT DOMAIN 21 115 Ig-like C2-type 1.
 FT DOMAIN 120 219 Ig-like C2-type 2.
 FT DOMAIN 224 304 Ig-like C2-type 3.
 FT DOMAIN 309 391 Ig-like C2-type 4.
 FT DOMAIN 395 497 Ig-like C2-type 5.
 FT MOTIF 146 148 Cell attachment site (Potential).
 FT CARBOHYD 140 140 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 298 298 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 481 481 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 42 100 By similarity.
 FT DISULFID 143 201 By similarity.
 FT DISULFID 245 288 By similarity.
 FT DISULFID 330 372 By similarity.
 FT DISULFID 416 482 By similarity.
 FT VAR_SEQ 118 136 Missing (in isoform 2).
 FT /FTId=VSP_011786.
 FT CONFLICT 48 48 R -> W (in Ref. 2).
 FT CONFLICT 166 166 G -> A (in Ref. 2).
 FT CONFLICT 376 376 P -> A (in Ref. 2).
 SQ SEQUENCE 700 AA; 74529 MW; 5D9404C2E13B18B8 CRC64;

Query Match 99.7%; Score 3678; DB 1; Length 700;
 Best Local Similarity 99.6%; Pred. No. 1.3e-224;
 Matches 697; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLASALLVFLCCFKGHAGSSPHFLQQPEDMVLLGEEARLPCALGAYRGLVQWTKDGLAL 60
 |||
 Db 1 MLASALLVFLCCFKGHAGSSPHFLQQPEDMVLLGEEARLPCALGAYRGLVQWTKDGLAL 60
 Qy 61 GGERDLPGWSRYWISGNSASGQHDHLHKPVELEDEASYECQASQAGLSRPAQLHVMVPP 120
 |||
 Db 61 GGERDLPGWSRYWISGNSASGQHDHLHKPVELEDEASYECQASQAGLSRPAQLHVMVPP 120
 Qy 121 EAPQVLGGPSVSLVAGVPGNLTCSRGRDSRPAPELLWFRDGI RL DASSFHQTTLKDKATG 180
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 Db 121 EAPQVLGGPSVSLVAGVPGNLTCSRGRDSRPAPELLWFRDGI RL DGSSFHQTTLKDKATG 180

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Qy      181 TVENTLFLTPSSHDDGATLICRARSQALPTGRDTAVTSLSLQYPPMVTLSAEPQTVQEGEK 240
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Db      181 TVENTLFLTPSSHDDGATLICRARSQALPTGRDTAVTSLSLQYPPMVTLSAEPQTVQEGEK 240

Qy      241 VTFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVDATFLTEPVSCVSNVAVGSANRS 300
        |||
Db      241 VTFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVDATFLTEPVSCVSNVAVGSANRS 300

Qy      301 TALEVLYGPILQAKPKSVSDVGKDASFSCVWRGNPLPRITWTRMGGSQVLSSGPTLRRLP 360
        |||
Db      301 TALEVLYGPILQAKPKSVSDVGKDASFSCVWRGNPLPRITWTRMGGSQVLSSGPTLRRLP 360

Qy      361 SVALEDAGDYVCRAEPRRTGLGGGKAQARLTVNAPPVVTALQPAPAFLRGPRLQCQVFA 420
        |||
Db      361 SVALEDAGDYVCRAEPRRTGLGGGKAQARLTVNAPPVVTALQPAPAFLRGPRLQCQVFA 420

Qy      421 SPAPDSVVWSWDEGFLEAGSLGRFLVEAFPAPEVEGGQGPGLISVLHISGTQESDFTTGF 480
        |||
Db      421 SPAPDSVVWSWDEGFLEAGSLGRFLVEAFPAPEVEGGQGPGLISVLHISGTQESDFTTGF 480

Qy      481 NCSARNRLGEGRVQIHLGRRDLLPTVRIVAGAASAATSLLMVITGVVLCCWRHGSLSKQK 540
        |||
Db      481 NCSARNRLGEGRVQIHLGRRDLLPTVRIVAGAASAATSLLMVITGVVLCCWRHGSLSKQK 540

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        |||
Db      541 NLVRIPGSSEGSSSRGPEEETGSSSEDRGPIVHTDHSDLVLEEKEALETKDPTNGYYRVRG 600

Qy      601 VSVSLSLGEAPGGGLFLPPPSPIGLPGTPTYDYDFKPHLDLVPPCRLYRARAGYLTPHPR 660
        |||
Db      601 VSVSLSLGEAPGGGLFLPPPSPIGLPGTPTYDYDFKPHLDLVPPCRLYRARAGYLTPHPR 660

Qy      661 AFTSYMKPTSFGPPDLSSGTPPFYATLSPPSHQRLQTHV 700
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Db      661 AFTSYMKPTSFGPPELSSGTPPFYATLSPPSHQRLQTHV 700
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